

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 29, 2003, 20:49:12 ; Search time 490.002 Seconds

(without alignments)
8229.920 Million cell updates/sec

Title: US-09-988-971-1_COPY_694_942

Sequence: 1 tggctgctatgagggccctgag.....agggccctgctgagccatcac 249

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_ges:*
18: em_ges_hum:*
19: em_ges_inv:*
20: em_ges_pln:*
21: em_ges_vrt:*
22: em_ges_fun:*
23: em_ges_mam:*
24: em_ges_mus:*
25: em_ges_other:*
26: em_ges_pro:*
27: em_ges_rod:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	247.4	99.4	1002 14	B0052308
2	238	95.6	1069 14	B0052468
3	236	94.8	1020 14	B0054281
4	213.8	85.9	926 11	AK020837
5	209.6	84.2	877 9	AL541041
6	163.4	65.6	377 9	AA959151

7	147	59.0	566	12	BG284179	BC384179	602408226
8	119.6	48.0	660	10	BB35615	BB35615	BB35615
9	107.2	43.1	966	14	B0054265	B0054265	B0054265
10	100.2	40.2	976	9	AL543079	AL543079	AL543079
11	100.2	40.2	1118	14	B0056298	B0056298	B0056298
12	99	39.8	627	10	BB619854	BB619854	BB619854
13	98.6	39.6	528	13	BI683002	BI683002	BI683002
14	98.6	39.6	521	13	BI345674	BI345674	BI345674
15	97	39.0	477	10	BE268290	BE268290	BE268290
16	97	39.0	783	13	BI820532	BI820532	BI820532
17	97	39.0	830	12	BE367639	BE367639	BE367639
18	97	39.0	996	14	BM919471	BM919471	BM919471
19	97	39.0	1055	14	BM918144	BM918144	BM918144
20	97	39.0	1192	13	BM545575	BM545575	BM545575
21	96.6	38.8	803	9	AI125413	AI125413	AI125413
22	95	38.2	800	13	BI839016	BI839016	BI839016
23	95	38.2	824	12	BF129084	BF129084	BF129084
24	95	38.2	998	12	BF129162	BF129162	BF129162
25	93	37.3	783	10	BE396636	BE396636	BE396636
26	90.2	36.2	390	10	AM487302	AM487302	AM487302
27	90	36.1	403	13	BI541790	BI541790	BI541790
28	89.8	36.1	916	12	BE745984	BE745984	BE745984
29	88.2	35.4	795	9	AL557199	AL557199	AL557199
30	88.2	35.4	1028	14	BM817288	BM817288	BM817288
31	88	35.3	558	13	BI681304	BI681304	BI681304
32	88	35.3	578	13	BI681042	BI681042	BI681042
33	87.6	35.2	891	14	B0051595	B0051595	B0051595
34	87.6	35.2	954	14	BQ711423	BQ711423	BQ711423
35	87.6	35.2	995	9	AL548206	AL548206	AL548206
36	87.6	35.2	1066	14	B0052951	B0052951	B0052951
37	86	34.5	862	13	BI819198	BI819198	BI819198
38	86	34.5	921	12	BE743960	BE743960	BE743960
39	85	34.1	1026	14	BQ62291	BQ62291	BQ62291
40	84.4	33.9	825	9	AL559108	AL559108	AL559108
41	84.2	33.8	2814	11	BC003253	BC003253	BC003253
42	82.6	33.2	286	14	R74940	R74940	R74940
43	82.6	33.2	539	13	BI900513	BI900513	BI900513
44	82.6	33.2	618	10	AM22890	AM22890	AM22890
45	82.6	33.2	693	14	BM949966	BM949966	BM949966

ALIGNMENTS

RESULT 1
LOCUS B0052308 1002 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT 6868571 NIH_MGC_106 Homo sapiens CDNA clone IMAGE:5933542
5' mRNA Sequence.
ACCESSION B0052308
VERSION B0052308.1 GI:19811648
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1002)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2118 row: d column: 23
High quality sequence stop: 670.
Location/Qualifiers
1..1002

FEATURES
source

into EcoRI/XhoI sites using the following 5' adaptor: GGCAACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using RAP-cDNA synthesis kit (Stratagene) and Bacteriophage II RT⁺ (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT	219 a	311 c	283 g	204 t	3 others
ORIGIN					

Query Match	94.8%;	Score 236;	DB 14;	Length 1020;
Best Local Similarity	98.8%;	Pred. No. 1.2e-54;		
Matches 247; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1

Qy 1 TGGCTGTATGAGGGCCCTGAGCAGCGAGAAAGCAGAGAACTGCTGTTTAACTGGGAAC 60

Db 491 TGGCTGATGAGGGCCCTGACGAGGAGAAAGCAGAGGAAGCTGCTGTTGTTAAGCTGCAAC 550

61 CCTGGAGGGGCTTCTCATCCGGAGAGCCAGACCAGGAGGGCTTACTCTGTCA 120

551 CTTGGAGGGGCTTCCTCATCCGGAGAGCCAGACAGGAGGCTCTTACTCTCTGCA 610

121 GTCCGCTCAGCCGCTGCACTCTGGACCGAICAGACACIACAGGATCAGCTT 180

501 GTCGCTCAGCCGCTTCGACCTGNGACCGAICAGACCTACAGGATCCATGCTT 600

[illegible]

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040

Db 731 GGACCAATTAC 740

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LOCUS	AK020837	926 bp	mRNA	linear	HTC 19-JAN-2002
DEFINITION	Mus musculus adult retina cDNA, RIKEN full-length enriched library,				

sequence.

VERSION AK020837.1 GI:12861542

SOURCE Mus musculus (strain: C57BL/6J) adult retina cDNA to mRNA

ORGANISM

REFERENCE
AUTHORS
1
Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

MEDLINE	99279253
PUBMED	10349636

REFERENCE AUTHORS

TITLE

JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)

PUBMED 11042159

AUTHORS

Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda Y., Tshikawa T., Ozawa K., Tanaka T., Matsuiwa S., Kawaji T.

JOURNAL Genome Res. 10 (11), 1557-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE
4 Kawai, T., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

Salto, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Salto, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,

TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21086660

REFERENCE
AUTHORS
5 (bases 1 to 926)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.

Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

FEATURES
sourceLocation/Qualifiers
1. .926/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="FANTOM DB:A930009E21"

/db_xref="MGI:MGI:1911678"

/db_xref="taxon:10090"

/clone="A930009E21"

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/dev_stage="adult"

128 - .667

/note="data source:SPRR, source key:Q60898, evidence:ISS"

putative

similar to SRC-LIKE ADAPTER PROTEIN"

/codon_start=1

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/db_xref="MGI:MGI:1925049"

/translation="MPSVYAKVAKHGMVLEGLSREKAEELLLDPNGAFILRESQT
RRCYSLSVLRSPASMDRIHRYLORLNDGMVYISPLRTPSLALVEHYSLDGI
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LRRESLSYSIADPPLDDA"

LRESLSYSIADPPLDDA"

907. .912

/note="putative"

polyA_signal

polyA_site

BASE COUNT 209 a 269 c 263 g 185 t

ORIGIN

Query Match

Best Local Similarity 91.2% Pred. No. 1.5e-48;

Matches 227; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TGCGTATAGAGGCTTGAGCAGGAGAGAAAGCAGAGAACTGCTGTTTACTCTGGAGAC 60

Db 164 TGCGTATAGAGGCTTGAGCAGGAGAGAAAGCAGAGAACTGCTGTTTACTCTGGAGAC 223

QY 61 CCTGAGAGGGGCTTCTCTATCGGAGAGCAGACAGGAGAGGCTTTACTCTGTCACA 120

Db 224 CCGGAGAGGGGCTTCTCTATCGGAGAGCAGACAGGAGAGGCTTTACTCTGTCACA 283

QY 121 GTCCGCTCAGCCGCCCTTGATCTCGGAGCCGAGTCACTACAGAGATCCACTGCCCTT 180

Db 284 GTCCGCTCAGCCGCCCTTGATCTCGGAGCCGAGTCACTACAGAGATCCACTGCCCTT 343

QY 181 GACATAGGCTGCTGATCATCTCAGCAGGCTCAGCTCCCTCAGCTCCAGGCTTGGTG 240

Db 344 GACATAGGCTGCTGATCATCTCAGCAGGCTCAGCTCCCTCAGCTCCAGGCTTGGTG 403

QY 241 GACCATTTAC 249

Db 404 GAGCATTTAC 412

RESULT 5

AL541041

LOCUS

DEFINITION

AL541041 LRT_FL002_PL1 Homo sapiens cDNA clone CS0005YK23 5 prime

AL541041 877 bp mRNA linear EST 16-FEB-2001

DEFINITION

AL541041 LRT_FL002_PL1 Homo sapiens cDNA clone CS0005YK23 5 prime

AL541041

AL541041.1 GI:12871733

EST.

human.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 877)

Li, W.-B., Gruber, C., Jessee, D. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

Location/Qualifiers

1. .877

/organism="Homo sapiens"

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/db_xref="MGI:MGI:1925049"

/db_xref="taxon:10090"

/issue_type="retina"

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/dev_stage="adult"

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/note="data source:SPRR, source key:Q60898, evidence:ISS"

putative

similar to SRC-LIKE ADAPTER PROTEIN"

/codon_start=1

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/db_xref="MGI:MGI:1925049"

/translation="MPSVYAKVAKHGMVLEGLSREKAEELLLDPNGAFILRESQT
RRCYSLSVLRSPASMDRIHRYLORLNDGMVYISPLRTPSLALVEHYSLDGI
CCPLREPCVLOKLGPIRGKDTPTPTVPTSLSWKKLDRSLIFLEAPASGEASLLISEG
LRRESLSYSIADPPLDDA"

LRESLSYSIADPPLDDA"

907. .912

/note="putative"

polyA_signal

polyA_site

BASE COUNT 192 a 262 c 251 g 170 t 2 others

ORIGIN

Query Match

Best Local Similarity 98.6% Pred. No. 2.2e-47;

Matches 209; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCGTATAGAGGCTTGAGCAGGAGAGAAAGCAGAGAACTGCTGTTTACTCTGGAGAC 60

Db 666 TGCGTATAGAGGCTTGAGCAGGAGAGAAAGCAGAGAACTGCTGTTTACTCTGGAGAC 725

QY 61 CCTGAGAGGGGCTTCTCTATCGGAGAGCAGACAGGAGAGGCTTTACTCTGTCACA 120

Db 726 CCGGAGAGGGGCTTCTCTATCGGAGAGCAGACAGGAGAGGCTTTACTCTGTCACA 785

QY 121 GTCCGCTCAGCCGCCCTTGATCTCGGAGCCGAGTCACTACAGAGATCCACTGCCCTT 180

Db 786 GTCCGCTCAGCCGCCCTTGATCTCGGAGCCGAGTCACTACAGAGATCCACTGCCCTT 845

QY 181 GACATAGGCTGCTGATCATCTCAGCAGGCTCAGCTCCCTCAGCTCCAGGCTTGGTG 240

Db 846 GACATAGGCTGCTGATCATCTCAGCAGGCTCAGCTCCCTCAGCTCCAGGCTTGGTG 403

RESULT 6

AA959151

LOCUS

DEFINITION

AA959151 v251906.r1 Soares thymus 2kbMT Mus musculus cDNA clone IMAGE:1330042 5' similar to TR:013239 PUTATIVE SRC-LIKE ADAPTER PROTEIN ; mRNA sequence.

AA959151

AA959151.1 GI:3124344

EST.

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 377)

Giesel, S., Kucada, T., Lacy, M., Le, M., Martin, D., Morris, B.,

Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,

Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Matern, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

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